ABSTRACT OF THE DISCLOSURE

A method and system for modeling a 3-dimensional structure of a protein using animation software techniques is provided. In one embodiment of the invention, the modeling is based upon identifying a 3-dimensional structure of a protein. Positional data regarding that 3-dimensional structure, more specifically, the X, Y and Z coordinates for the structure, are generated. Using these coordinates, an animation software, such as MEL (Maya Embedded Language) Script or "melscript" is employed that uses the coordinates to create an image of animation information to be displayed on a computer screen, or other visual medium. Further refinement techniques are used to improve the accuracy of the representation in animation. The model of the protein is thereby generated as an animation of the protein and it can be displayed and evaluated accordingly.

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